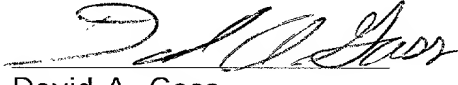


IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Alitalo *et al.* ) EXPRESS MAIL LABEL NO.:  
Serial No.: Not yet assigned ) EM578445010US  
Filed: Herewith ) I hereby certify that this paper and  
For: Flt4 (VEGFR-3) as a Target ) the documents referred to as  
for Tumor Imaging and Anti-Tumor ) enclosed herewith are being  
Therapy ) deposited with the United States  
Group Art Unit: Not yet assigned ) Postal Service as "EXPRESS MAIL  
Examiner: Not yet assigned ) POST OFFICE TO ADDRESSEE"  
 ) Service under 37 C.F.R. §1.10 on  
 ) the date indicated below and is  
 ) addressed to: Commissioner for  
 ) Patents, Box Patent Application,  
 ) Washington, D.C. 20231 on this  
 ) date:  
 )  
 ) January 19, 2001  
 )  
 )   
 ) David A. Gass

STATEMENT PURSUANT TO 37 C.F.R. § 1.921(f)

Commissioner for Patents  
Box Patent Application  
Washington, D.C. 20231

Sir:

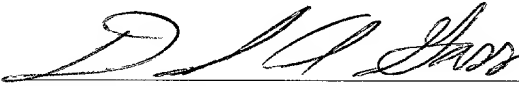
I hereby state that the content of the paper and computer readable forms of the sequence listing that is part of the above-identified application and that are filed herewith are the same.

Respectfully submitted,

MARSHALL, O'TOOLE, GERSTEIN,  
MURRAY & BORUN  
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233 South Wacker Drive  
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January 19, 2001

By:

  
David A. Gass  
Reg. No: 38,153

SEQUENCE LISTING

<110> Alitalo, Kari  
Kaipainen, Arja  
Valtola, Reija  
Jussila, Lotta

<120> Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Therapy

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Glu	Ser	Thr	Glu	Val 325	Ile	Val	His	Glu	Asn 330	Pro	Phe	Ile	Ser	Val 335	Glu
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Val Ser Gln His Asp Leu Gly Ser Tyr Val Cys Lys Ala Asn Asn Gly	
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Phe Ile Ser Val Glu Trp Leu Lys Gly Pro Ile Leu Glu Ala Thr Ala	
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Gly Asp Glu Leu Val Lys Leu Pro Val Lys Leu Ala Ala Tyr Pro Pro	
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Lys Leu Ser Ile Gln Arg Val Arg Glu Glu Asp Ala Gly Arg Tyr Leu	
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Glu	Ser	Ile	Phe	Asp	Lys	Val	Tyr	Thr	Thr	Gln	Ser	Asp	Val	Trp	Ser	
		1085				1090				1095						
ttt	ggg	gtg	ctt	ctc	tgg	gag	atc	ttc	tct	ctg	ggg	gcc	tcc	ccg	tac	3364
Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	Gly	Ala	Ser	Pro	Tyr	
1100				1105				1110				1115				
cct	ggg	gtg	cag	atc	aat	gag	gag	ttc	tgc	cag	cgg	ctg	aga	gac	ggc	3412
Pro	Gly	Val	Gln	Ile	Asn	Glu	Glu	Phe	Cys	Gln	Arg	Leu	Arg	Asp	Gly	
		1120						1125				1130				
aca	agg	atg	agg	gcc	ccg	gag	ctg	gcc	act	ccc	gcc	ata	cgc	cgc	atc	3460
Thr	Arg	Met	Arg	Ala	Pro	Glu	Leu	Ala	Thr	Pro	Ala	Ile	Arg	Arg	Ile	
		1135						1140				1145				
atg	ctg	aac	tgc	tgg	tcc	gga	gac	ccc	aag	gcg	aga	cct	gca	ttc	tcg	3508
Met	Leu	Asn	Cys	Trp	Ser	Gly	Asp	Pro	Lys	Ala	Arg	Pro	Ala	Phe	Ser	
		1150				1155				1160						
gag	ctg	gtg	gag	atc	ctg	ggg	gac	ctg	ctc	cag	ggc	agg	ggc	ctg	caa	3556
Glu	Leu	Val	Glu	Ile	Leu	Gly	Asp	Leu	Leu	Gln	Gly	Arg	Gly	Leu	Gln	
		1165				1170				1175						
gag	gaa	gag	gag	gtc	tgc	atg	gcc	ccg	cgc	agc	tct	cag	agc	tca	gaa	3604
Glu	Glu	Glu	Glu	Val	Cys	Met	Ala	Pro	Arg	Ser	Ser	Gln	Ser	Ser	Glu	
1180				1185				1190				1195				
gag	ggc	agc	ttc	tcg	cag	gtg	tcc	acc	atg	gcc	cta	cac	atc	gcc	cag	3652
Glu	Gly	Ser	Phe	Ser	Gln	Val	Ser									

gct gac gct gag gac agc ccg cca agc ctg cag cgc cac agc ctg gcc 3700  
Ala Asp Ala Glu Asp Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala  
1215 1220 1225

gcc agg tat tac aac tgg gtg tcc ttt ccc ggg tgc ctg gcc aga ggg 3748  
Ala Arg Tyr Tyr Asn Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly  
1230 1235 1240

gct gag acc cgt ggt tcc tcc agg atg aag aca ttt gag gaa ttc ccc 3796  
Ala Glu Thr Arg Gly Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro  
1245 1250 1255

atg acc cca acg acc tac aaa ggc tct gtg gac aac cag aca gac agt 3844  
Met Thr Pro Thr Thr Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser  
1260 1265 1270 1275

ggg atg gtg ctg gcc tgc gag gag ttt gag cag ata gag agc agg cat 3892  
Gly Met Val Leu Ala Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His  
1280 1285 1290

aga caa gaa agc ggc ttc agc tgt aaa gga cct ggc cag aat gtg gct 3940  
Arg Gln Glu Ser Gly Phe Ser Cys Lys Gly Pro Gly Gln Asn Val Ala  
1295 1300 1305

gtg acc agg gca cac cct gac tcc caa ggg agg cgg cgg cgg cct gag 3988  
Val Thr Arg Ala His Pro Asp Ser Gln Gly Arg Arg Arg Arg Pro Glu  
1310 1315 1320

cgg ggg gcc cga gga ggc cag gtg ttt tac aac agc gag tat ggg gag 4036  
Arg Gly Ala Arg Gly Gly Gln Val Phe Tyr Asn Ser Glu Tyr Gly Glu  
1325 1330 1335

ctg tgc gag cca agc gag gag gac cac tgc tcc ccg tct gcc cgc gtg 4084  
Leu Ser Glu Pro Ser Glu Glu Asp His Cys Ser Pro Ser Ala Arg Val  
1340 1345 1350 1355

act ttc ttc aca gac aac agc tac taagcagcat cggacaagac cccagcact 4138  
Thr Phe Phe Thr Asp Asn Ser Tyr  
1360

tgggggttca ggcccggcag ggcgggcaga gggctggagg cccaggctgg gaactcatct 4198

ggttgaactc tgggtggcaca ggagtgtcct cttccctctc tgcagacttc ccagctagga 4258

agagcaggac tccaggccca aggctcccgg aattccgtca ccacgactgg ccagggcacg 4318

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gtgctggtcc cggggccagc acttccatgg gaatgtctct ttggcgacct cctttcatca 4438

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gcacacagct actctcccca cgagggtgg ctggcctcac ccaccctgc acagttgaag 4618

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aaacagccaa ctagccccctg ggggtggccac cagtatgaca gtattatacg ctggcaacac 4738

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<213> Homo sapiens

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Asn Ile Thr Glu Glu Ser His Val Ile Asp Thr Gly Asp Ser Leu Ser  
35 40 45  
Ile Ser Cys Arg Gly Gln His Pro Leu Glu Trp Ala Trp Pro Gly Ala  
50 55 60  
Gln Glu Ala Pro Ala Thr Gly Asp Lys Asp Ser Glu Asp Thr Gly Val  
65 70 75 80  
Val Arg Asp Cys Glu Gly Thr Asp Ala Arg Pro Tyr Cys Lys Val Leu  
85 90 95  
Leu Leu His Glu Val His Ala Asn Asp Thr Gly Ser Tyr Val Cys Tyr  
100 105 110  
Tyr Lys Tyr Ile Lys Ala Arg Ile Glu Gly Thr Thr Ala Ala Ser Ser  
115 120 125  
Tyr Val Phe Val Arg Asp Phe Glu Gln Pro Phe Ile Asn Lys Pro Asp  
130 135 140  
Thr Leu Leu Val Asn Arg Lys Asp Ala Met Trp Val Pro Cys Leu Val  
145 150 155 160  
Ser Ile Pro Gly Leu Asn Val Thr Leu Arg Ser Gln Ser Ser Val Leu  
165 170 175  
Trp Pro Asp Gly Gln Glu Val Val Trp Asp Asp Arg Arg Gly Met Leu  
180 185 190  
Val Ser Thr Pro Leu Leu His Asp Ala Leu Tyr Leu Gln Cys Glu Thr  
195 200 205  
Thr Trp Gly Asp Gln Asp Phe Leu Ser Asn Pro Phe Leu Val His Ile  
210 215 220  
Thr Gly Asn Glu Leu Tyr Asp Ile Gln Leu Leu Pro Arg Lys Ser Leu  
225 230 235 240  
Glu Leu Leu Val Gly Glu Lys Leu Val Leu Asn Cys Thr Val Trp Ala  
245 250 255  
Glu Phe Asn Ser Gly Val Thr Phe Asp Trp Asp Tyr Pro Gly Lys Gln  
260 265 270

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Ala	Glu	Arg	Gly	Lys	Trp	Val	Pro	Glu	Arg	Arg	Ser	Gln	Gln	Thr	His		
	275						280					285					
Thr	Glu	Leu	Ser	Ser	Ile	Leu	Thr	Ile	His	Asn	Val	Ser	Gln	His	Asp		
	290					295					300						
Leu	Gly	Ser	Tyr	Val	Cys	Lys	Ala	Asn	Asn	Gly	Ile	Gln	Arg	Phe	Arg		
305					310					315					320		
Glu	Ser	Thr	Glu	Val	Ile	Val	His	Glu	Asn	Pro	Phe	Ile	Ser	Val	Glu		
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Trp	Leu	Lys	Gly	Pro	Ile	Leu	Glu	Ala	Thr	Ala	Gly	Asp	Glu	Leu	Val		
			340					345					350				
Lys	Leu	Pro	Val	Lys	Leu	Ala	Ala	Tyr	Pro	Pro	Pro	Glu	Phe	Gln	Trp		
		355					360					365					
Tyr	Lys	Asp	Gly	Lys	Ala	Leu	Ser	Gly	Arg	His	Ser	Pro	His	Ala	Leu		
	370					375					380						
Val	Leu	Lys	Glu	Val	Thr	Glu	Ala	Ser	Thr	Gly	Thr	Tyr	Thr	Leu	Ala		
385					390					395					400		
Leu	Trp	Asn	Ser	Ala	Ala	Gly	Leu	Arg	Arg	Asn	Ile	Ser	Leu	Glu	Leu		
				405					410					415			
Val	Val	Asn	Val	Pro	Pro	Gln	Ile	His	Glu	Lys	Glu	Ala	Ser	Ser	Pro		
			420					425					430				
Ser	Ile	Tyr	Ser	Arg	His	Ser	Arg	Gln	Ala	Leu	Thr	Cys	Thr	Ala	Tyr		
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Gly	Val	Pro	Leu	Pro	Leu	Ser	Ile	Gln	Trp	His	Trp	Arg	Pro	Trp	Thr		
	450					455					460						
Pro	Cys	Lys	Met	Phe	Ala	Gln	Arg	Ser	Leu	Arg	Arg	Arg	Gln	Gln	Gln		
465					470					475					480		
Asp	Leu	Met	Pro	Gln	Cys	Arg	Asp	Trp	Arg	Ala	Val	Thr	Thr	Gln	Asp		
				485					490					495			
Ala	Val	Asn	Pro	Ile	Glu	Ser	Leu	Asp	Thr	Trp	Thr	Glu	Phe	Val	Glu		
			500					505					510				
Gly	Lys	Asn	Lys	Thr	Val	Ser	Lys	Leu	Val	Ile	Gln	Asn	Ala	Asn	Val		
		515					520					525					
Ser	Ala	Met	Tyr	Lys	Cys	Val	Val	Ser	Asn	Lys	Val	Gly	Gln	Asp	Glu		
	530					535					540						
Arg	Leu	Ile	Tyr	Phe	Tyr	Val	Thr	Thr	Ile	Pro	Asp	Gly	Phe	Thr	Ile		
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Glu	Ser	Lys	Pro	Ser	Glu	Glu	Leu	Leu	Glu	Gly	Gln	Pro	Val	Leu	Leu		
				565					570					575			

Ser Cys Gln Ala Asp Ser Tyr Lys Tyr Glu His Leu Arg Trp Tyr Arg  
580 585 590

Leu Asn Leu Ser Thr Leu His Asp Ala His Gly Asn Pro Leu Leu Leu  
595 600 605

Asp Cys Lys Asn Val His Leu Phe Ala Thr Pro Leu Ala Ala Ser Leu  
610 615 620

Glu Glu Val Ala Pro Gly Ala Arg His Ala Thr Leu Ser Leu Ser Ile  
625 630 635 640

Pro Arg Val Ala Pro Glu His Glu Gly His Tyr Val Cys Glu Val Gln  
645 650 655

Asp Arg Arg Ser His Asp Lys His Cys His Lys Lys Tyr Leu Ser Val  
660 665 670

Gln Ala Leu Glu Ala Pro Arg Leu Thr Gln Asn Leu Thr Asp Leu Leu  
675 680 685

Val Asn Val Ser Asp Ser Leu Glu Met Gln Cys Leu Val Ala Gly Ala  
690 695 700

His Ala Pro Ser Ile Val Trp Tyr Lys Asp Glu Arg Leu Leu Glu Glu  
705 710 715 720

Lys Ser Gly Val Asp Leu Ala Asp Ser Asn Gln Lys Leu Ser Ile Gln  
725 730 735

Arg Val Arg Glu Glu Asp Ala Gly Arg Tyr Leu Cys Ser Val Cys Asn  
740 745 750

Ala Lys Gly Cys Val Asn Ser Ser Ala Ser Val Ala Val Glu Gly Ser  
755 760 765

Glu Asp Lys Gly Ser Met Glu Ile Val Ile Leu Val Gly Thr Gly Val  
770 775 780

Ile Ala Val Phe Phe Trp Val Leu Leu Leu Leu Ile Phe Cys Asn Met  
785 790 795 800

Arg Arg Pro Ala His Ala Asp Ile Lys Thr Gly Tyr Leu Ser Ile Ile  
805 810 815

Met Asp Pro Gly Glu Val Pro Leu Glu Glu Gln Cys Glu Tyr Leu Ser  
820 825 830

Tyr Asp Ala Ser Gln Trp Glu Phe Pro Arg Glu Arg Leu His Leu Gly  
835 840 845

Arg Val Leu Gly Tyr Gly Ala Phe Gly Lys Val Val Glu Ala Ser Ala  
850 855 860

Phe Gly Ile His Lys Gly Ser Ser Cys Asp Thr Val Ala Val Lys Met  
865 870 875 880

Leu Lys Glu Gly Ala Thr Ala Ser Glu His Arg Ala Leu Met Ser Glu  
885 890 895

Leu Lys Ile Leu Ile His Ile Gly Asn His Leu Asn Val Val Asn Leu  
 900 905 910  
 Leu Gly Ala Cys Thr Lys Pro Gln Gly Pro Leu Met Val Ile Val Glu  
 915 920 925  
 Phe Cys Lys Tyr Gly Asn Leu Ser Asn Phe Leu Arg Ala Lys Arg Asp  
 930 935 940  
 Ala Phe Ser Pro Cys Ala Glu Lys Ser Pro Glu Gln Arg Gly Arg Phe  
 945 950 955 960  
 Arg Ala Met Val Glu Leu Ala Arg Leu Asp Arg Arg Arg Pro Gly Ser  
 965 970 975  
 Ser Asp Arg Val Leu Phe Ala Arg Phe Ser Lys Thr Glu Gly Gly Ala  
 980 985 990  
 Arg Arg Ala Ser Pro Asp Gln Glu Ala Glu Asp Leu Trp Leu Ser Pro  
 995 1000 1005  
 Leu Thr Met Glu Asp Leu Val Cys Tyr Ser Phe Gln Val Ala Arg Gly  
 1010 1015 1020  
 Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala  
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 Arg Asn Ile Leu Leu Ser Glu Ser Asp Val Val Lys Ile Cys Asp Phe  
 1045 1050 1055  
 Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly  
 1060 1065 1070  
 Ser Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asp  
 1075 1080 1085  
 Lys Val Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu  
 1090 1095 1100  
 Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Gln Ile  
 1105 1110 1115 1120  
 Asn Glu Glu Phe Cys Gln Arg Leu Arg Asp Gly Thr Arg Met Arg Ala  
 1125 1130 1135  
 Pro Glu Leu Ala Thr Pro Ala Ile Arg Arg Ile Met Leu Asn Cys Trp  
 1140 1145 1150  
 Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe Ser Glu Leu Val Glu Ile  
 1155 1160 1165  
 Leu Gly Asp Leu Leu Gln Gly Arg Gly Leu Gln Glu Glu Glu Val  
 1170 1175 1180  
 Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu Glu Gly Ser Phe Ser  
 1185 1190 1195 1200  
 Gln Val Ser Thr Met Ala Leu His Ile Ala Gln Ala Asp Ala Glu Asp  
 1205 1210 1215

Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala Ala Arg Tyr Tyr Asn  
1220 1225 1230

Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly Ala Glu Thr Arg Gly  
1235 1240 1245

Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro Met Thr Pro Thr Thr  
1250 1255 1260

Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala  
265 1270 1275 1280

Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His Arg Gln Glu Ser Gly  
1285 1290 1295

Phe Ser Cys Lys Gly Pro Gly Gln Asn Val Ala Val Thr Arg Ala His  
1300 1305 1310

Pro Asp Ser Gln Gly Arg Arg Arg Arg Pro Glu Arg Gly Ala Arg Gly  
1315 1320 1325

Gly Gln Val Phe Tyr Asn Ser Glu Tyr Gly Glu Leu Ser Glu Pro Ser  
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Glu Glu Asp His Cys Ser Pro Ser Ala Arg Val Thr Phe Phe Thr Asp  
345 1350 1355 1360

Asn Ser Tyr

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Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro  
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Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr  
35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro  
50 55 60

Glu Asn Asn Asn Asn Asn Met Val Ser Lys Glu Ser Glu Arg Leu  
65 70 75 80

Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser  
85 90 95

Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn His Thr Gly Phe Tyr Ser  
100 105 110

Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser  
115 120 125

105110 4455360



Ala	Ile	Tyr	Ile	Phe	Ile	Ser	Asp	Thr	Gly	Arg	Pro	Phe	Val	Glu	Met
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Tyr	Ser	Glu	Ile	Pro	Glu	Ile	Ile	His	Met	Thr	Glu	Gly	Arg	Glu	Leu
145					150					155					160
Val	Ile	Pro	Cys	Arg	Val	Thr	Ser	Pro	Asn	Ile	Thr	Val	Thr	Leu	Lys
				165					170					175	
Lys	Phe	Pro	Leu	Asp	Thr	Leu	Ile	Pro	Asp	Gly	Lys	Arg	Ile	Ile	Trp
			180					185					190		
Asp	Ser	Arg	Lys	Gly	Phe	Ile	Ile	Ser	Asn	Ala	Thr	Tyr	Lys	Glu	Ile
		195					200					205			
Gly	Leu	Leu	Thr	Cys	Glu	Ala	Thr	Val	Asn	Gly	His	Leu	Tyr	Lys	Thr
	210					215					220				
Asn	Asn	Tyr	Leu	Thr	His	Arg	Gln	Thr	Asn	Thr	Ile	Ile	Asp	Val	Gln
225					230					235					240
Ile	Ser	Thr	Pro	Arg	Pro	Val	Lys	Leu	Leu	Arg	Gly	His	Thr	Leu	Val
				245					250					255	
Leu	Asn	Cys	Thr	Ala	Thr	Thr	Pro	Leu	Asn	Thr	Arg	Val	Gln	Met	Thr
			260					265					270		
Trp	Ser	Tyr	Pro	Asp	Asn	Asn	Asn	Glu	Lys	Asn	Lys	Arg	Ala	Ser	Val
		275					280					285			
Arg	Arg	Arg	Ile	Asp	Gln	Ser	Asn	Ser	His	Ala	Asn	Ile	Phe	Tyr	Ser
	290					295					300				
Val	Leu	Thr	Ile	Asp	Lys	Met	Gln	Asn	Lys	Asp	Lys	Gly	Leu	Tyr	Thr
305					310					315					320
Cys	Arg	Val	Arg	Ser	Gly	Pro	Ser	Phe	Lys	Ser	Val	Asn	Thr	Ser	Val
				325					330					335	
His	Ile	Tyr	Asp	Lys	Ala	Phe	Ile	Thr	Val	Lys	His	Arg	Lys	Gln	Gln
			340					345					350		
Val	Leu	Glu	Thr	Val	Ala	Gly	Lys	Arg	Ser	Tyr	Arg	Leu	Ser	Met	Lys
		355					360					365			
Val	Lys	Ala	Phe	Pro	Ser	Pro	Glu	Val	Val	Trp	Leu	Lys	Asp	Gly	Leu
	370					375					380				
Pro	Ala	Thr	Glu	Lys	Ser	Ala	Arg	Tyr	Leu	Thr	Arg	Gly	Tyr	Ser	Leu
385					390					395					400
Ile	Ile	Lys	Asp	Val	Thr	Glu	Glu	Asp	Ala	Gly	Asn	Tyr	Thr	Ile	Leu
				405					410					415	
Leu	Ser	Ile	Lys	Gln	Ser	Asn	Val	Phe	Lys	Asn	Leu	Thr	Ala	Thr	Leu
			420					425					430		
Ile	Val	Asn	Val	Lys	Pro	Gln	Ile	Tyr	Glu	Lys	Ala	Val	Ser	Ser	Phe
		435					440					445			

Pro	Asp	Pro	Ala	Leu	Tyr	Pro	Leu	Gly	Ser	Arg	Gln	Ile	Leu	Thr	Cys
450						455					460				
Thr	Ala	Tyr	Gly	Ile	Pro	Gln	Pro	Asn	Thr	Ile	Lys	Trp	Phe	Trp	His
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Pro	Cys	Asn	His	Asn	His	Ser	Glu	Ala	Arg	Cys	Asp	Phe	Cys	Ser	Asn
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Asn	Glu	Glu	Ser	Phe	Ile	Leu	Asp	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Ala
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Asp	Ser	Asn	Met	Gly	Asn	Arg	Ile	Glu	Ser	Ile	Thr	Gln	Arg	Met	Ala
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Ile	Ile	Glu	Gly	Lys	Asn	Lys	Met	Ala	Ser	Thr	Leu	Val	Val	Ala	Asp
	530					535					540				
Ser	Arg	Ile	Ser	Gly	Ile	Tyr	Ile	Cys	Ile	Ala	Ser	Asn	Lys	Val	Gly
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Thr	Val	Gly	Arg	Asn	Ile	Ser	Phe	Tyr	Ile	Thr	Asp	Val	Pro	Asn	Gly
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Phe	His	Val	Asn	Leu	Glu	Lys	Met	Pro	Thr	Asn	Asn	Glu	Gly	Glu	Asp
			580					585					590		
Leu	Lys	Leu	Ser	Cys	Thr	Val	Asn	Lys	Phe	Leu	Tyr	Arg	Asp	Val	Thr
		595					600					605			
Trp	Ile	Leu	Leu	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn
	610					615						620			
Asn	Asn	Asn	Asn	Asn	Arg	Thr	Val	Asn	Asn	Arg	Thr	Met	His	Tyr	Ser
625					630					635					640
Ile	Ser	Lys	Gln	Lys	Met	Ala	Ile	Thr	Lys	Glu	His	Ser	Ile	Thr	Leu
				645					650					655	
Asn	Leu	Thr	Ile	Met	Asn	Val	Ser	Leu	Gln	Asp	Ser	Gly	Thr	Tyr	Ala
			660					665					670		
Cys	Arg	Ala	Arg	Asn	Val	Tyr	Thr	Gly	Glu	Glu	Ile	Leu	Gln	Lys	Lys
		675					680					685			
Glu	Ile	Thr	Ile	Arg	Asp	Gln	Glu	Ala	Pro	Tyr	Leu	Leu	Arg	Asn	Leu
	690					695					700				
Ser	Asp	His	Thr	Val	Ala	Ile	Ser	Ser	Ser	Thr	Thr	Leu	Asp	Cys	His
705					710					715					720
Ala	Asn	Gly	Val	Pro	Glu	Pro	Gln	Ile	Thr	Trp	Phe	Lys	Asn	Asn	His
				725					730					735	
Lys	Ile	Gln	Gln	Glu	Pro	Gly	Ile	Ile	Leu	Gly	Pro	Gly	Ser	Ser	Thr
			740					745					750		
Leu	Phe	Ile	Glu	Arg	Val	Thr	Glu	Glu	Asp	Glu	Gly	Val	Tyr	His	Cys
		755					760					765			

Lys	Ala	Thr	Asn	Gln	Lys	Gly	Ser	Val	Glu	Ser	Ser	Ala	Tyr	Leu	Thr
770						775					780				
Val	Gln	Gly	Thr	Ser	Asp	Lys	Ser	Asn	Leu	Glu	Leu	Ile	Thr	Leu	Thr
785					790					795					800
Cys	Thr	Cys	Val	Ala	Ala	Thr	Leu	Phe	Trp	Leu	Leu	Leu	Thr	Leu	Leu
				805					810					815	
Ile	Arg	Lys	Met	Lys	Arg	Ser	Ser	Asn	Ser	Glu	Ile	Lys	Thr	Asp	Tyr
			820					825					830		
Leu	Ser	Ile	Ile	Met	Asp	Pro	Asp	Glu	Val	Pro	Leu	Asp	Glu	Gln	Cys
		835					840					845			
Glu	Arg	Leu	Pro	Tyr	Asp	Ala	Ser	Lys	Trp	Glu	Phe	Ala	Arg	Glu	Arg
850						855					860				
Leu	Lys	Leu	Gly	Lys	Ser	Leu	Gly	Arg	Gly	Ala	Phe	Gly	Lys	Val	Val
865					870					875					880
Gln	Ala	Ser	Ala	Phe	Gly	Ile	Lys	Lys	Ser	Pro	Thr	Cys	Arg	Thr	Val
				885					890					895	
Ala	Val	Lys	Met	Leu	Lys	Glu	Gly	Ala	Thr	Ala	Ser	Glu	Tyr	Lys	Ala
			900					905					910		
Leu	Met	Thr	Glu	Leu	Lys	Ile	Leu	Thr	His	Ile	Gly	His	His	Leu	Asn
		915					920					925			
Val	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Lys	Gln	Gly	Gly	Pro	Leu	Met
930						935					940				
Val	Ile	Val	Glu	Tyr	Cys	Lys	Tyr	Gly	Asn	Leu	Ser	Asn	Tyr	Leu	Lys
945					950					955					960
Ser	Lys	Arg	Asp	Leu	Phe	Phe	Leu	Asn	Lys	Asp	Ala	Ala	Leu	His	Met
				965					970					975	
Glu	Pro	Lys	Lys	Glu	Lys	Met	Glu	Pro	Gly	Leu	Glu	Gln	Gly	Lys	Lys
			980					985					990		
Pro	Arg	Leu	Asp	Ser	Val	Thr	Ser	Ser	Glu	Ser	Phe	Ala	Ser	Ser	Gly
		995					1000					1005			
Phe	Gln	Glu	Asp	Lys	Ser	Leu	Ser	Asp	Val	Glu	Glu	Glu	Glu	Asp	Ser
1010						1015					1020				
Asp	Gly	Phe	Tyr	Lys	Glu	Pro	Ile	Thr	Met	Glu	Asp	Leu	Ile	Ser	Tyr
1025				1030						1035					1040
Ser	Phe	Gln	Val	Ala	Arg	Gly	Met	Glu	Phe	Leu	Ser	Ser	Arg	Lys	Cys
			1045					1050						1055	
Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Leu	Ser	Glu	Asn	Asn
		1060					1065						1070		
Val	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Tyr	Lys	Asn
	1075						1080					1085			

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<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence
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<220>
<223> The amino acid at positions 1 and 2 each are
selected independently from the group consisting
of aspartic acid and glutamic acid.

<220>
<223> The amino acid at position 4 is independently
selected from the group consisting of methionine
and valine.
```

<220>  
 <223> The amino acid at position 5 is independently  
 selected from the group consisting of proline,  
 aspartic acid, and glutamic acid.

<220>  
 <223> Description of Artificial Sequence: consensus  
 sequence

<400> 6  
 Xaa Xaa Tyr Xaa Xaa Met  
 1 5

<210> 7  
 <211> 70  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide probe

<400> 7  
 acatgcatgc caccatgcag cggggcgccg cgctgtgcct gcgactgtgg ctctgcctgg 60  
 gactcctgga 70

<210> 8  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide probe

<400> 8  
 acatgcatgc cccgccggtc atcc 24

<210> 9  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide probe

<400> 9  
 cggaattccc catgacccca ac 22

<210> 10  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

459260

<220>

<223> Description of Artificial Sequence:  
oligonucleotide probe

<400> 10

ccatcgatgg atcctacctg aagccgcttt ctt

33

<210> 11

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide probe

<400> 11

cccaagcttg gatccaagtg gctactccat gacc

34

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide probe

<400> 12

gttgccctgtg atgtgcacca

20

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide probe

<400> 13

ctggagtcga cttggcggac t

21

<210> 14

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide probe

<400> 14

cgcggatccc tagtgatggt gatggtgatg totaccttcg atcatgctgc ccttatactc 60

<210> 15  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide probe

<400> 15  
ctggagtcga cttggcggac t 21

<210> 16  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
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oligonucleotide probe

<400> 16  
cgggatccct ccatgctgcc cttatcct 28

<210> 17  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
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oligonucleotide probe

<400> 17  
ggcaagcttg aattcgccac catgcagcgg ggcgcc 36

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide probe

<400> 18  
gttgctgtg atgtgcacca 20

<210> 19  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide probe

21

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<210> 20
<211> 44
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence:  
oligonucleotide probe

44

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<210> 21
<211> 419
<212> PRT
<213> Homo sapiens
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<400> 21
Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
  1             5             10             15
```

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe  
20 25 30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala  
35 40 45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser  
50 55 60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met  
65 70 75 80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln  
85 90 95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala  
100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys  
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe  
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr  
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr  
165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu  
180 185 190



Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser  
195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile  
210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn  
225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys  
245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser  
260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu  
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys  
290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys  
305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu  
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro  
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys  
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr  
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser  
385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro  
405 410 415

Gln Met Ser

<210> 22  
<211> 354  
<212> PRT  
<213> Homo sapiens

<400> 22  
Met Tyr Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val  
1 5 10 15

Gln Leu Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser  
20 25 30

CCF046360

Ser	Gln	Ser	Thr	Leu	Glu	Arg	Ser	Glu	Gln	Gln	Ile	Arg	Ala	Ala	Ser
		35					40					45			
Ser	Leu	Glu	Glu	Leu	Leu	Arg	Ile	Thr	His	Ser	Glu	Asp	Trp	Lys	Leu
	50					55					60				
Trp	Arg	Cys	Arg	Leu	Arg	Leu	Lys	Ser	Phe	Thr	Ser	Met	Asp	Ser	Arg
	65				70					75					80
Ser	Ala	Ser	His	Arg	Ser	Thr	Arg	Phe	Ala	Ala	Thr	Phe	Tyr	Asp	Ile
				85					90					95	
Glu	Thr	Leu	Lys	Val	Ile	Asp	Glu	Glu	Trp	Gln	Arg	Thr	Gln	Cys	Ser
			100					105					110		
Pro	Arg	Glu	Thr	Cys	Val	Glu	Val	Ala	Ser	Glu	Leu	Gly	Lys	Ser	Thr
		115					120					125			
sn	Thr	Phe	Phe	Lys	Pro	Pro	Cys	Val	Asn	Val	Phe	Arg	Cys	Gly	Gly
	130					135					140				
Cys	Cys	Asn	Glu	Glu	Ser	Leu	Ile	Cys	Met	Asn	Thr	Ser	Thr	Ser	Tyr
	145				150					155					160
Ile	Ser	Lys	Gln	Leu	Phe	Glu	Ile	Ser	Val	Pro	Leu	Thr	Ser	Val	Pro
				165					170					175	
Glu	Leu	Val	Pro	Val	Lys	Val	Ala	Asn	His	Thr	Gly	Cys	Lys	Cys	Leu
			180					185					190		
Pro	Thr	Ala	Pro	Arg	His	Pro	Tyr	Ser	Ile	Ile	Arg	Arg	Ser	Ile	Gln
		195					200					205			
Ile	Pro	Glu	Glu	Asp	Arg	Cys	Ser	His	Ser	Lys	Lys	Leu	Cys	Pro	Ile
	210					215					220				
Asp	Met	Leu	Trp	Asp	Ser	Asn	Lys	Cys	Lys	Cys	Val	Leu	Gln	Glu	Glu
	225				230					235					240
Asn	Pro	Leu	Ala	Gly	Thr	Glu	Asp	His	Ser	His	Leu	Gln	Glu	Pro	Ala
				245					250					255	
Leu	Cys	Gly	Pro	His	Met	Met	Phe	Asp	Glu	Asp	Arg	Cys	Glu	Cys	Val
			260					265					270		
Cys	Lys	Thr	Pro	Cys	Pro	Lys	Asp	Leu	Ile	Gln	His	Pro	Lys	Asn	Cys
		275					280					285			
Ser	Cys	Phe	Glu	Cys	Lys	Glu	Ser	Leu	Glu	Thr	Cys	Cys	Gln	Lys	His
	290					295					300				
Lys	Leu	Phe	His	Pro	Asp	Thr	Cys	Ser	Cys	Glu	Asp	Arg	Cys	Pro	Phe
	305				310					315					320
His	Thr	Arg	Pro	Cys	Ala	Ser	Gly	Lys	Thr	Ala	Cys	Ala	Lys	His	Cys
				325					330					335	
Arg	Phe	Pro	Lys	Glu	Lys	Arg	Ala	Ala	Gln	Gly	Pro	His	Ser	Arg	Lys
			340					345					350		

Asn Pro

Figure 1 consists of 12 histograms arranged in a single column. Each histogram represents the distribution of the number of non-zero elements in the vector  $x$  for a specific value of  $n$ . The x-axis for all histograms is labeled 'Number of non-zero elements' and ranges from 0 to 120. The y-axis is labeled 'Frequency' and ranges from 0 to 100. The histograms are for  $n = 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120$ . As  $n$  increases, the distribution of non-zero elements shifts to the right, indicating that more elements in the vector  $x$  are non-zero for larger  $n$ . The peak frequency of the distributions decreases as  $n$  increases.